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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=7; day=8; hr=8; min=28; sec=28; ms=260;]

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Application No: 09370453 Version No: 3.0

Input Set:

Output Set:

Started: 2008-07-08 08:22:04.146
Finished: 2008-07-08 08:22:06.742
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 596 ms
Total Warnings: 65
Total Errors: 0
No. of SeqIDs Defined: 77
Actual SeqID Count: 77

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (26)
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Input Set:

Output Set:

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Denney, Jr., Dan W.

<120> Vaccines for Treatment of Lymphoma and Leukemia

<130> GENITOPE-03849

<140> 09370453

<141> 2008-07-08

<160> 77

<170> PatentIn version 3.3

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<213> Artificial Sequence

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<223> Synthetic

<400> 2

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<210> 3

<211> 677

<212> DNA

<213> Simian virus 40

<400> 3

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<213> Homo sapiens

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23

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 <222> (88)..(741)

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1	5		
att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct		162	
Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro			
10	15	20	25
aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg		210	
Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu			
30	35	40	
att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg		258	
Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met			
45	50	55	
gga ggc cat cac att gtg gcc ctc tgt gtg ctc aag ggg ggc tat aag		306	
Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr Lys			
60	65	70	
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Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser			
75	80	85	
gat aga tcc att cct atg act gta gat ttt atc aga ctg aag agc tac		402	
Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser Tyr			
90	95	100	105
tgt aat gat cag tca acg ggg gac ata aaa gtt att ggt gga gat gat		450	
Cys Asn Asp Gln Ser Thr Gly Asp Ile Lys Val Ile Gly Gly Asp Asp			
110	115	120	
ctc tca act tta act gga aag aat gtc ttg att gtt gaa gat ata att		498	
Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile Ile			
125	130	135	
gac act ggt aaa aca atg caa act ttg ctt tcc ctg gtt aag cag tac		546	
Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr			
140	145	150	
agc ccc aaa atg gtt aag gtt gca agc ttg ctg gtg aaa agg acc tct		594	
Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser			
155	160	165	
cga agt gtt gga tac agg cca gac ttt gtt gga ttt gaa att cca gac		642	
Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp			
170	175	180	185
aag ttt gtt gga tat gcc ctt gac tat aat gag tac ttc agg aat		690	
Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn			
190	195	200	
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Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys			
205	210	215	

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Ala

gccagtaaaa tttagcaggtg ttcttagtcct gtggccatct gcctagtaaa gcttttgca 851
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<211> 218
<212> PRT
<213> Mus musculus

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20 25 30

Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
50 55 60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
65 70 75 80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
130 135 140

Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
165 170 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
180 185 190

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195 200 205

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<213> Mus musculus

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<222> (13)..(573)

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99

Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg

15 20 25

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147

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30 35 40 45

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195

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50 55 60

cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt

243

Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser

65 70 75

aga gaa ctc aaa gaa cca cca cga gga gct cat ttt ctt gcc aaa agt

291

Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser

80 85 90

ttg gat gat gcc tta aga ctt att gaa caa ccg gaa ttg gca agt aaa

339

Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys

95 100 105

gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc

387

Val Asp Met Val Trp Ile Val Gly Ser Ser Val Tyr Gln Glu Ala

110 115 120 125

atg aat caa cca ggc cac ctt aga ctc ttt gtg aca agg atc atg cag

435

Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln

130 135 140

gaa ttt gaa agt gac acg ttt ttc cca gaa att gat ttg ggg aaa tat

483

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85																95
Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val A																